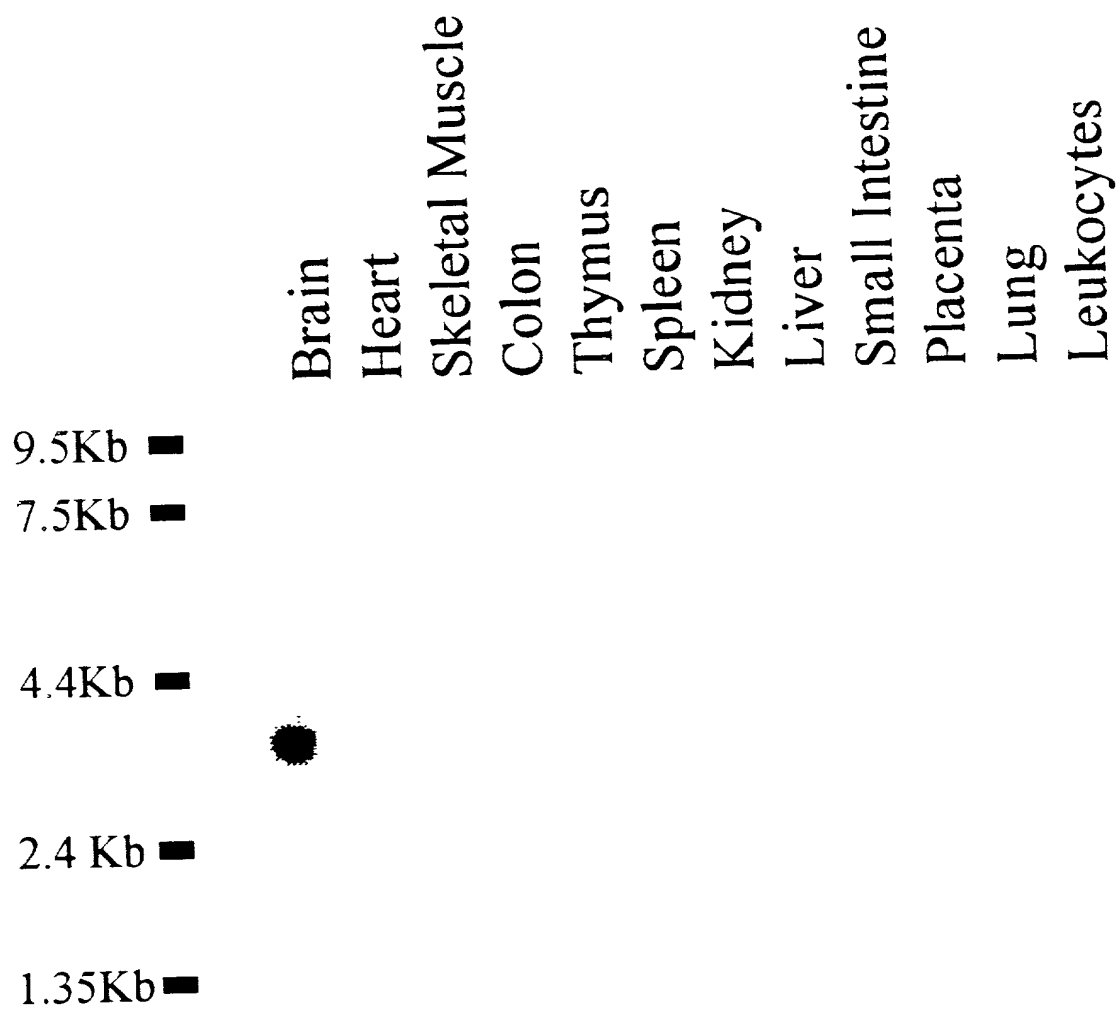


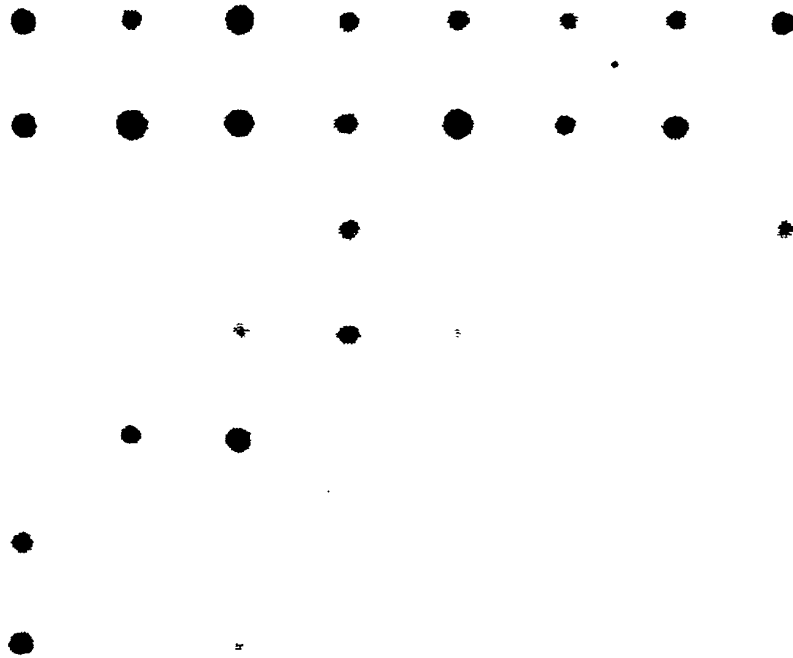
1 MEA--EQAAGASEGATPGLAVPVA~~PPAT~~-----hHac3.pro  
1 -----hHac2.pro  
1 MARGGGRGESPGATPA~~PGPPPP~~~~PPAP~~~~PGPGPAPPQHPPRAEALPPEAADEGGPRGR~~hHac1.pro  
32 -----AASGP-----hHac3.pro  
1 -----hHac2.pro  
61 LRSRDSSCGRPGTPGAATAKSPNGECGRGEPQCSPAGPEGPARGPKVSFSCRGAASGP-----hHac1.pro  
37 IEKSGP-----EBK-----RRHLGTLLOPTVKNKFSLRVFGSHKAVEIEQEhHac3.pro  
1 -----KEQE-----hHac2.pro  
121 AEGPGEAAEAGSEAGPAC~~EP~~RGSQASFMQ~~Q~~FGALLQBGVNKFSLRMFGSOKAVEREQEhHac1.pro  
77 RVKSAGAWIIHPYSDFRYWDLIMLIMVGNLIIVLPVGITFFKEENSPPWIVFNVLSDTFhHac3.pro  
5 RVKTAGFWIIHPYSDFRYWDLIMLIMVGNLIIVIPVGITFFTEQTTPWIIIFNVASDTVhHac2.pro  
181 RVKSAGAWIIHPYSDFRYWDFTMLIFMVGNLIIPVGITFFKDETAPWIVFNVLSDTFhHac1.pro  
137 FLDDLVLNFRGTGIVVEGAELIAERARTRYLRTWELVDLSSIPVDYIFLVELEPRLhHac3.pro  
65 FLDDLIMNFRGTGIMNEDSEIILDEKVIMN~~Y~~LKSWFVVDFISSIPVDYIFLIVEKG--MhHac2.pro  
241 FLDDLVLNFRGTGIVIEDNTEIILDEKIKKYLRTWFWVD~~EM~~SSIPVDYIFLIVEKG--IhHac1.pro  
197 DAEVYKTARALRIVRFTKILSLLRLLRSLRILIRYIHQWEEIFHMTYDLASAVVRIFNLIghHac3.pro  
123 DSEVYKTARALRIVRFTKILSLLRLLRSLRILIRYIHQWEEIFHMTYDLASAVVRIFNLIghHac2.pro  
299 DSEVYKTARALRIVRFTKILSLLRLLRSLRILIRYIHQWEEIFHMTYDLASAVMRICNLIshHac1.pro  
257 MMLLLCHWDFCLQFLVPMLQDFPPDCWVSINHMVNHSWGRQYSHALFKAMSHMLCIGYQhHac3.pro  
183 MMLLLCHWDFCLQFLVPLQDFPPDCWVSINEMVN~~D~~SWGKQYSYALFKAMSHMLCIGYGAhHac2.pro  
359 MMLLLCHWDFCLQFLVPMLQDFPNCWVSINCMVNHSWSELYSFALFKAMSHMLCIGYGRhHac1.pro  
317 QAPVGM~~PD~~WLTMLSMIVGATCYAMFIGHATALIQSLDSSRRRQYQEKYQVEQYMSFHKLhHac3.pro  
243 QAPVMS~~DL~~WLTMLSMIVGATCYAMFVGHATALIQSLDSSRRRQYQEKYQVEQYMSFHKLhHac2.pro  
419 QAPFS~~MT~~WLTMLSMIVGATCYAMFIGHATALIQSLDSSRRRQYQEKYQVEQYMSFHKLhHac1.pro

FIG. 1A.

377	PADTRQRIHEIYEYEHRYQGKMFDEESILGELSEPLREEIINFTCRGLVAHMPLEFAHADPSF	hHac3.pro
303	PADMRQKIHDYEHRYQGKIIFDEENIINELNDPLREEIVNFCRKLVAITMPLFANADPNF	hHac2.pro
479	PADFRQKIHDYEHRYQGKMFDEDSILGELNGPLREEIVNFCRKLVASMPLEFANADPNF	hHac1.pro
437	VTAMLTKLRFEFVQPGDLVVREGSVGRKMYFIZHGLLSVLARGARDTRLTDGSYFGEICL	hHac3.pro
363	VTAMLTKLRFEFVQPGDYIIREGAVGKKMYFIZHGVAGVITTKSSKEMKLTDDGSYFGEICL	hHac2.pro
539	VTAMLTKLRFEFVQPGDYIIREGTIGKKMYFIZHGVSVLTGKNGEMKLSDDGSYFGEICL	hHac1.pro
497	LTRGRRRTASVRADTYCRLYSLSDVDFHFNALVEEFPMRRRAFETVAMDRLIRIGKKNSILQR	hHac3.pro
423	LTRGRRRTASVRADTYCRLYSLSDVDFNEVLEEYPMRRRAFETVAIDRLDRIGKKNSILIQ	hHac2.pro
599	LTRGRRRTASVRADTYCRLYSLSDVDFNEVLEEYPMRRRAFETVAIDRLDRIGKKNSILIH	hHac1.pro
557	R-RSEPSPG--SSGGIMEHLVQHDRDMARGVGRAPSTGAQLSGKPVLWEPLVHAPLQ	hHac3.pro
483	KFKQKDLNTGVFNQENELTKQIVKHDREMVQAIAPINYPQMTILNSTSTTTETSRMRTQ	hHac2.pro
459	KVQHDNLNSGVFNQENALITQELVKVDREMVQQA---ELGQRVGL-----	hHac1.pro
613	AAATSNVAIALTHQRGPIPLSP-DSPATLARSAMRSAGSPA--SPLVPVR--AGPW	hHac3.pro
543	SPPVYATATSLSHSNLHSPSTQTQPSAILSPCSYTTAVCSPPMOQSPIAARTFHYASPT	hHac2.pro
700	-----FPPPPPPPPQVTSATATLQQA-AMSFCEQVARELVGP-LALGSPR	hHac1.pro
666	ASTSRLEAF-PARTLHASLSRAAGRSQVSLGPPPGGG-----GRRIGPR	hHac3.pro
603	ASQLSLMQQQPQQVQSSQPQRQQQF-SPPQPTPGSSTPKNEVHKSTQAIHNTNLTRE	hHac2.pro
743	LVRPPPGGAPAAASPGRPASPSPGAFASPRAPRTSPYGGLPAAAPLAGPALPARRLSRA	hHac1.pro
709	GRPLSASQPSLPQRAITCDGSPGRKSGS-ERI-----PPSGILAKPPRTAQPP--	hHac3.pro
662	VRPESAMQPSLPHEVS--TLISRPHPTVCELSIASIPQPVTAVPGTGLQAGGRSTVPQRV	hHac2.pro
803	SRPLSASQPSLPHGAPCPAASRTREASSTPRLGPTPAARAAPSPDRRDSASPGAAGGL-	hHac1.pro
756	--RPPVPPEATPRGLQLSANM.	hHac3.pro
720	FFRQMSSGAIPENRGVLPAPPLITPHPKK	hHac2.pro
862	-----DEQDSARSLSSNL.	hHac1.pro

FIG. 1B.

*FIG. 2A.*



whole brain	amygdala	caudate nucleus	cerebellum	cerebral cortex	frontal lobe	hippocampus	medulla oblongata
occipital lobe	putamen	substantia nigra	temporal lobe	thalamus	nucleus accumbens	spinal cord	
heart	aorta	skeletal muscle	colon	bladder	uterus	prostate	stomach
testis	ovary	pancreas	pituitary gland	adrenal gland	thyroid gland	salivary gland	mammary gland
kidney	liver	small intestine	spleen	thymus	peripheral leukocyte	lymph node	bone marrow
appendix	lung	trachea	placenta				
fetal brain	fetal heart	fetal kidney	fetal liver	fetal spleen	fetal thymus	fetal lung	

FIG. 2B.

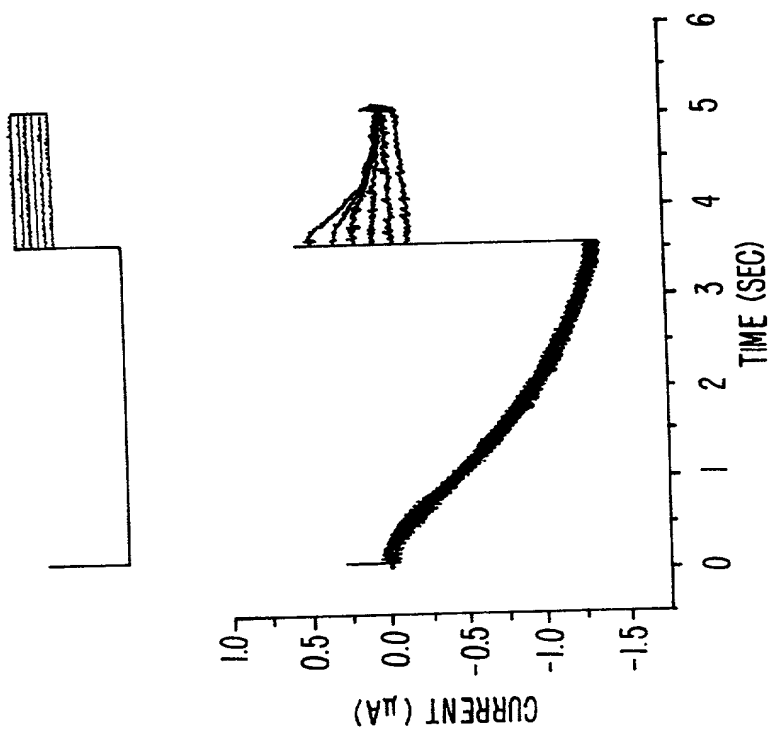


FIG. 3A.

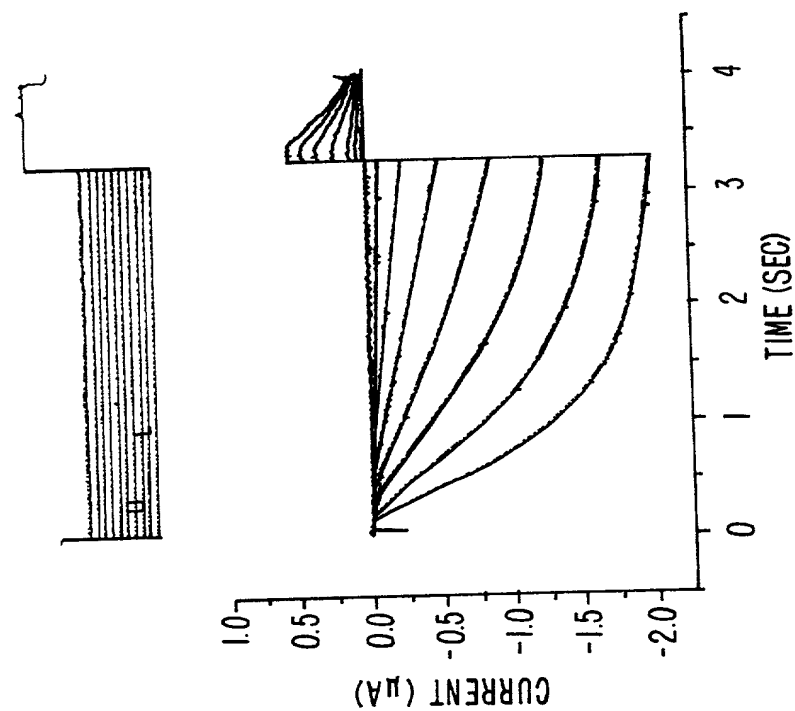
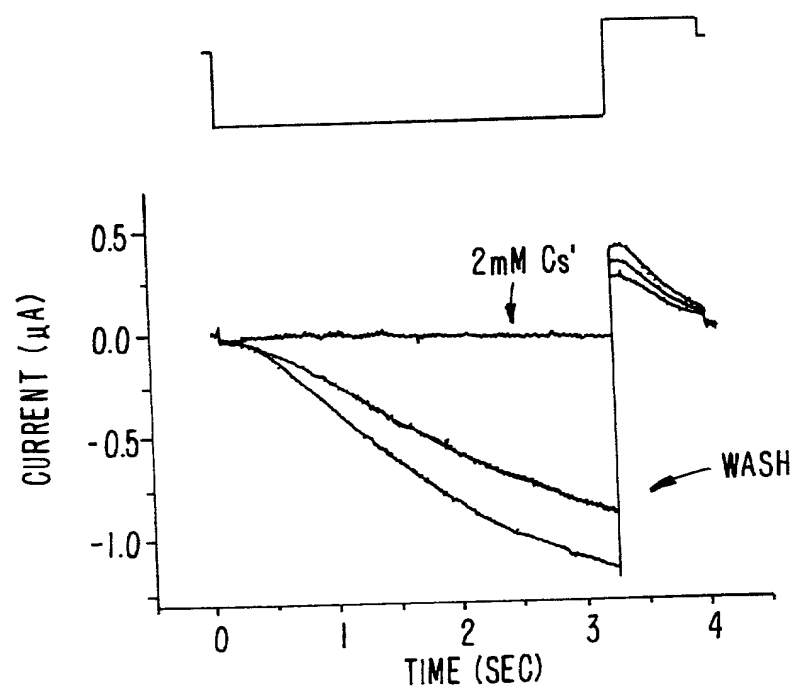


FIG. 3B.

*FIG. 4.*